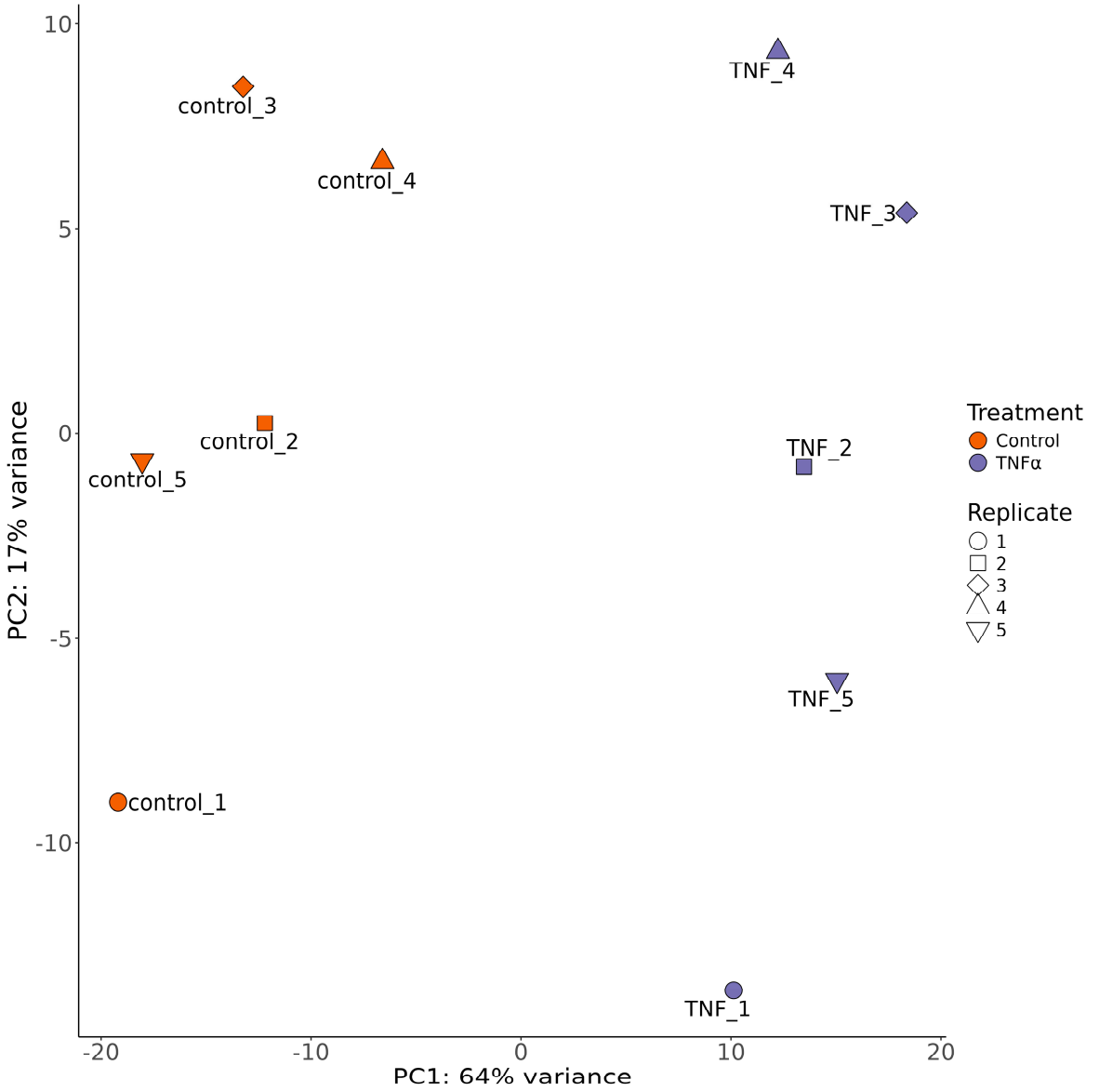



**Figure S1**. Graphical representation of the first (PC1; culture time) and second (PC2; treatment) principal components (PC) affecting gene expression profile in equine endometrial fibroblasts (n=5) after 96 hours of TNF$\alpha$ treatment (10 ng/mL). Control: control cells, untreated; TNF$\alpha$: cells treated with TNF$\alpha$; 1, 2, 3, 4, 5: biological replicates.

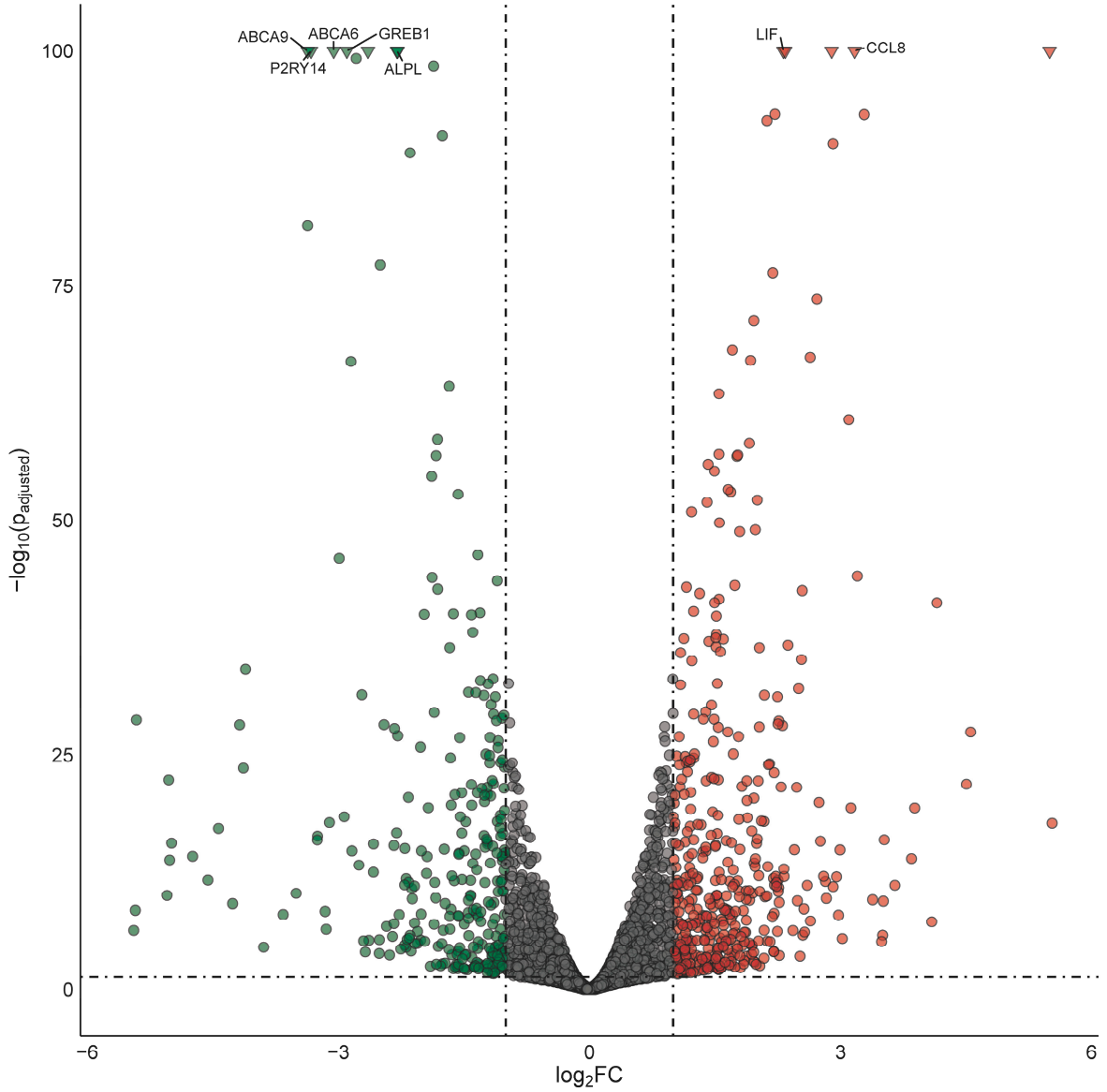



**Figure S2**. Volcano plot presenting differentially expressed genes (DEGs; the established criteria: $p_{adjusted}<0.05$; log2 fold change (log2FC)≥1.0/log2FC≤-1.0; determined by DESeq2 package [version 1.42.0] within R statistical software) identified in equine endometrial fibroblasts (n=5) after 96 hours of TNF$\alpha$ treatment (10 ng/mL). Differentially expressed genes are represented by multicolored circles, where red color means up-regulated DEGs and green color depicts down-regulated DEGs. The grey circles represent all remaining transcripts identified in the examined samples. Triangles depict values outside the coordinate system.

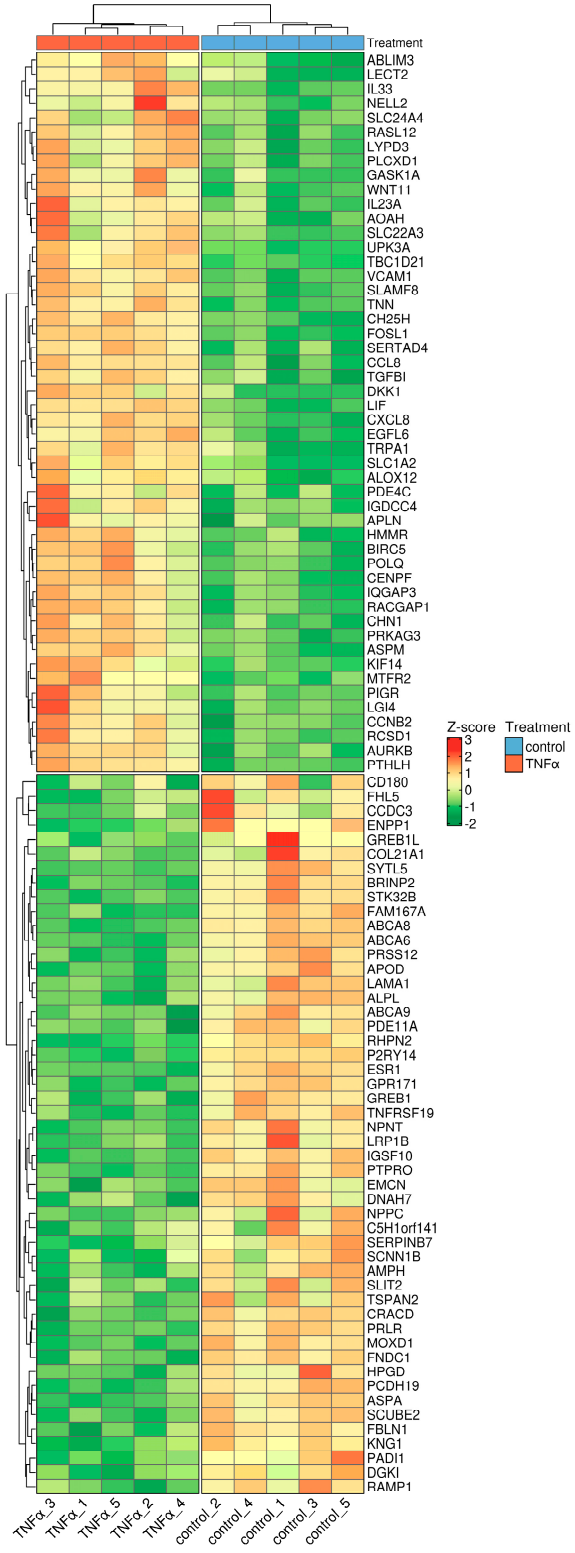



**Figure S3**. Heatmap illustrating the expression profile of top 100 differentially expressed genes (DEGs; the established criteria: $p_{adjusted}<0.05$; log2 fold change (log2FC)≥1.0/log2FC≤-1.0; determined by DESeq2 package [version 1.42.0] within R statistical software) identified in equine endometrial fibroblasts (n=5) after 96 hours of TNF$\alpha$ treatment (10 ng/mL). The color scale of the heatmaps represents the expression level, where the red blocks represent up-regulated DEGs, and the green blocks represent down-regulated DEGs. control: control cells, untreated; TNF$\alpha$: cells treated with TNF$\alpha$ (10 ng/mL); 1, 2, 3, 4, 5: biological replicates.